

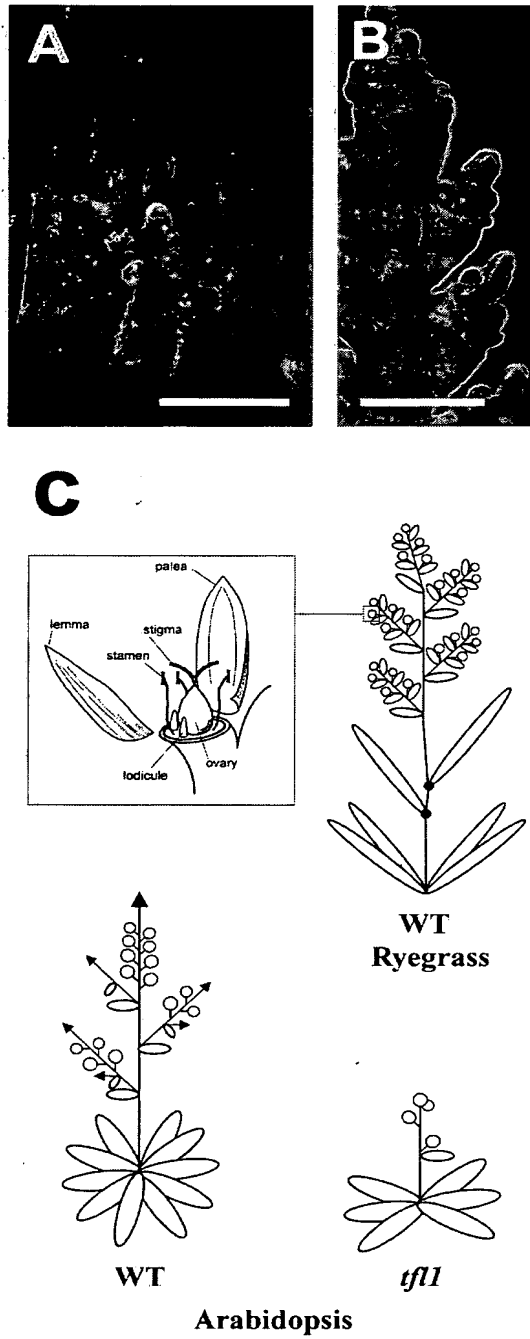
FIGURE 1

FIGURE 2

		GCC	-76
-75	CAAGCCACTTCAAAGCTTTGCTACTACCAGATAGAGCATTACCGTGCAATATAGAAATACTTGCCTCTCCAACC		-1
1	ATGTCTAGGTCTGTGGAGCCTCTTATTGTTGGTCGTGTCATTGGAGAAGTTCTCGATCCATTTAACCCATGTGTG		75
76	AAGATGGTAGCAACCTATAACTCAAACAAGCTGGTCTTCAATGGTCATGAGCTCTACCCATCAGCAGTTGTATCT		150
151	AAACCAAGAGTAGAGGTTCAAGGGGGTGACTTGCGATCCTTATTCACATTGGTTATGACGGACCCAGATGTGCCA		225
226	GGACCAAGTGATCCGTATCTGCGGGAGCATCTTCACTGGATTGTCAGTAATATACCTGGGACAACAGATGCTTCA		300
301	TTTGGGGGGGAGGTCATGAGCTATGAGAGCCCAAAGCCCAACATTGGAATCCACAGGTTCAATTTTGTGCTCTTC		375
375	AAGCAGAAGCGAAGGCAGACTGTATCTGTGCCTTCCTTCAGGGATCATTTCAACACCCGCCAGTTTGCTGTGGAT		450
451	AATGATCTTGGCCTCCCTGTGGCTGCTGTTTACTTCAATTGTCAGAGAGAGACTGCTGCCAGGAGGCCTGAAAA		525
526	TCGAGTTCTTGGCTATCCAGTTGTGCCAAATAAAGGCTTTTGGAGTTATGCACCTTCTTTCTGAAGTCAATGCT		600
601	CCTCTTCTACATTACTTCCTCGTGGACCATTGCTTCTTTACTACAGTTTTTGTCTCAGGGATCAAATAAATCAAGT		675
675	GCATTTTGGAGATTGTATTAGATTATATTGTAAGCAGTGAGATCAGCAACCATGTGTTAACATAAGCCAGTACAT		750
751	TAGCAGGTCCATGTTTATGGTTTCATGTTGTGTGTAAGCAGTTATCACTAGAAAGGAAGGTCAGGTAGACAACCCA		825
826	AACTGGCAAAAAAAGCTTTATCTA		851

FIGURE 3

-3600 cactagtaacggccgcccagtggtgctggaattcagggttaatacgcactcactatagggmgctcgaggatcttcccac -3526
 -3525 cagtgtgcattcatgtgttacttaccactctccaacttgagggactcaagattggtgggcccgtccttttcgctg -3451
 -3450 aagcgatccaaaggtgtcgggtaacgggttatgacagcaaacagaaacatcgccatctgcacggaagccagaagt -3376
 -3375 agttactatgtcaaagggatataaaaaactcactaatgaagggggatgctattgctgagataaaactgctatctca -3301
 -3300 tctacaggtgagattgcaagtatacttgacaacagggccagatgggtatggcatgaagaaaattagggctggagta -3226
 -3225 gaaaggtgaagatagcatggatttggatgagatggctagagggttgcgagatatcaaatagaagacacttcttca -3151
 -3150 atgattcaatagaagatgcatgtgccattacagagtggattattatgtcctttttaaagagatgcttacgtccct -3076
 -3075 gacctttctataacacaaattacactcctttgctagacttttctgctataattgtctttcctcgccaaaagaat -3001
 -3000 aatactatagaacttcttaatttaatttcccttattttcttgactctatcttaattctcctcctattgttcag -2926
 -2925 ccaaggactgctccttccatttacttgccgacagggtgactgacaaatgacacctgcgcgtttgtgatcaagag -2851
 -2850 cctgaatctatttctcacctcatgctgcaatgctccttctcacagcaaatatggtatgatctgcagtaagctc -2776
 -2775 aaccttctgccaatgtatgccagttggcaacgccgagttcagcatttgggttcgcccagctgcccgaacgctcaa -2701
 -2700 ccagccctgcagaaggggtgctaaatccatcatcatccttactctctggagattatggaagacgaggaacgatgct -2626
 -2625 atcttcaaaaatctggccccaacagactgccttagttcagtcgatcctagatgaagcctgtcaatggtcgta -2551
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 -2475 gtctaactaagtttagccctgtacagtttttttctcttttctcttttcttttttcttttctcttctttctgtt -2401
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 -2325 gcatgtgttcgagaaaaaatttacttacctcttaggctatattctcttcaccaacttgactccacaaagcttc -2251
 -2250 aatcgcaacttgtccaagctgctgccgctggtgctgctgctccttttccaatgcatccatacactgtcctagtca -2176
 -2175 cataccaaacaaaaaagctaattgccgcccctgttgtttcaaatgaattatctgattgtgatgctgctaattcttt -2101
 -2100 gcatatgagctcgcggcatatgaatgaacttggtttggcagaatgaacaaagagaggacttcttgatggatata -2026
 -2025 cactggtaaagctgaagttctgtgagcaggctatgatgttccctgttataaaaaaggctatgaaaaacttgtgat -1951
 -1950 aggtgttaagattggttttattttgcgtgcaaatgggttcagtggaagttgtagtgtcactagctgtgtggtg -1876
 -1875 ctactgtgctaccaacacactgtagcactgccaaaaatttatgaaaaagttctgaacagacgagatgtatctatca -1801
 -1800 attcatggacccattttgttataattttcttttaaaaaataaaatccgtaaagaatcaataagtggaattattg -1726
 -1725 gaaatgaaaaaagtaaccaaataactaaacttttttcaatacagatcgatatcatggagacacactggctac -1651
 -1650 cattggttggaatagctactagattccactacagctagggtgtcaagcaactataatggcatcagaatggagcaga -1576
 -1575 aaaatgtcacaaagctgtacttactccactacttctagctgcacaaatgtcaagcaggcatgattgcactagacc -1501
 -1500 agaacatagtaatgcataaagctgtaattggctccactacttatggaacgaagaaatctattattttattgtttt -1426
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 -1125 aacatttgagggtgaagaggcttccacgtggacagtgcgcgatgtttctgtccactagataaacacctaataata -1051
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 -975 caaaaacgaattgatagtttaggaaagcatcactccaaagtgttttattcccgttcttttctattgtctccacaa -901
 -900 gggcacttctctaaatttctgcgaacaattacatctagatctttttaaactgaagtatttttagcatgaaaacg -826
 -825 cattgttctgtaattgtggtgtgaatttcgactgctcatctgatttccctctggtagaatacataaataattat -751
 -750 acacaacagcatgataatgtgcaaaactaagcatcaaaatctgcacattgtcatgcagaaactaggacaggagga -676
 -675 ccagcactttgtcggttcttaaccaatattaacatagtttcagcaacataatcttcagagaccactagcatga -601
 -600 aggtgtgttatgtttcctaaagaaataacatgtaggtagtgatctacaataccttttttggggactataaggtgg -526
 -525 gaaacctcaacttgaaaaggtttccatttaatacaagtataaaaaaacagtattttttaactatcaataactaaaa -451
 -450 ttaaaacagaatagagatatatacaaatgaaaatcaaacagttgtgcaaatgtatttatcgtagtttagtatct -376
 -375 catgtttctggtgaaaaaattctctgcccttagaacttgaagaagatgcatgaagtattactccaaactccaac -301
 -300 actgtgcaactgatagaaaagaacaagaccttgggttggtgtctcggaaaaagtggttaggtcctttctgtgg -226
 -225 ccttttcagttctttccacgcataaccaacaaaaaagaacacagatactactcatgtctcacattctcttttga -151
 -150 gcttacactcgaagcaggcttcttgccctctataagtagaggctcgctgactctagcaatgctcagtaagcaGCC -76
 -75 **CAAGCCACTTCAAAGCTTTGCTACTACCAGATAGAGCATTCACCGTGCAATATAGAAATACTTGCCCTCTCCAAAC** -1
 1 **ATGTCTAGGTCTGTGGAGCCTCTTATTGTTGGTTCGCTGTCATTGGAGAAGTTCTCGATCCATTTAACCATGTGTG** 75
 76 **AAGATGGTAGCAACCTATAACTCAAACAAGCTGGTCTTCAATGGTCATGAGCTCTACCCATCAGCAGTTGTATCT** 150
 151 **AAACCAAGAGTAGAGGTTTCAGGGGGTGACTTGGCATCCTTATTCACATTG**gtagaatgcactcgactcgatcctt 225
 226 ggaactccatattcaacttcgagtattgtatgcttgttttcttcttctcgcagtgccataattattcatatttca 300
 301 **gGTTATGACGGACCCAGATGTGCCAGGACCAAGTGATCCGTATCTGCGGGAGCATCTTCACTGGT**aacctttctc 375
 375 atgcacagtttttctgctgggtggctactaagcacctaaatatattagatatatttttttgaaaggaaaaatatat 450

451	tagtatatgttgctaaggaatatagaagtacatcttcttcttgccacatatatagacagagagactattttaatatag	525
526	cacttctaacgagaggtcatttaccataaccttttacacttacacaggATTGTCAGTAATATACCTGGGACAACAG	600
601	ATGCTTCATTTGGtaggtccttctctgagatttgaattggtatattctatgttctgcattttgaatgaataacca	675
675	ctgaccttttgaattgcaggGGGGGAGGTCATGAGCTATGAGAGCCCAAAGCCCAACATTGGAATCCACAGGTTT	750
751	ATTTTTGTGCTCTTCAAGCAGAAGCGAAGGCAGACTGTATCTGTGCCTTCCTTCAGGGATCATTTCAACACCCGC	825
826	CAGTTTGTGCTGTGGATAATGATCTTGGCCTCCCTGTGGCTGCTGTTTACTTCAATTGTCAGAGAGAGACTGCTGCC	900
901	AGGAGGCGCTGAAAAATCGAGTTCTTGGCTATCCAGTTGTGCCAAATAAAGGCTTTTGGAGTTATGCACCTTCTT	975
976	TCTGAAGTCAATGCTCCTCTTCTACATTACTTCCTCGTGGACCATTGCTTCTTTACTACAGTTTTTGTCTAGGGA	1050
1051	TCAAATAAATCAAGTGCAATTTTGGAGATTGTATTAGATTATATTGTAAGCAGTGAGATCAGCAACCATGTGTTAA	1125
1126	CATAAGCCAGTACATTAGCAGGTCCATGTTTATGGTTTCATGTTGTGTGTAAGCAGTTATCACTAGAAAGGAAGGT	1200
1201	CAGGTAGACAACCCAAACTGGCAAAAAAAAAAGCTTTATCTActgtatggcccttgccggccttgatgttccatgc	1275
1276	accttttctgacatgctgtctactgtatgccaccgccactataatgtatgagatatgaatataaaatggagatat	1350
1351	ccaaaatatccagatgattgcccactaaatgctaaatgtacatagtggttttccacctatgttgcattcatcat	1425
1426	gtccttacacaaaatcagaaaacatccatttcatgcacattgatgcacactgcatattaacaatctattcagatt	1500
1501	tggtgttaaacacacccttattttccgcatccattaatattatatttagtaccctggacaggttaagccttttgag	1575
1576	cacagtaagtaaccggatgaaattacaatatgatcctcgagcgccctat	1624

FIGURE 4

1	MSRSVEPLIVGRVIGEVLDPFNPCVKMVATYNSNKLVFNGHELYPSAVVSKPRVEVQGGDLRLSLFTLVMTDPDVP	75
76	GPSDPYLRHLHWIVSNIPGTTDASFGGEVMSYESPKPNIGIHRFIFVLFKQRRQTTSVPSFRDHFNTROFAVD	150
151	NDLGLPVAAVYFNCQRETAARRR	173

FIGURE 5

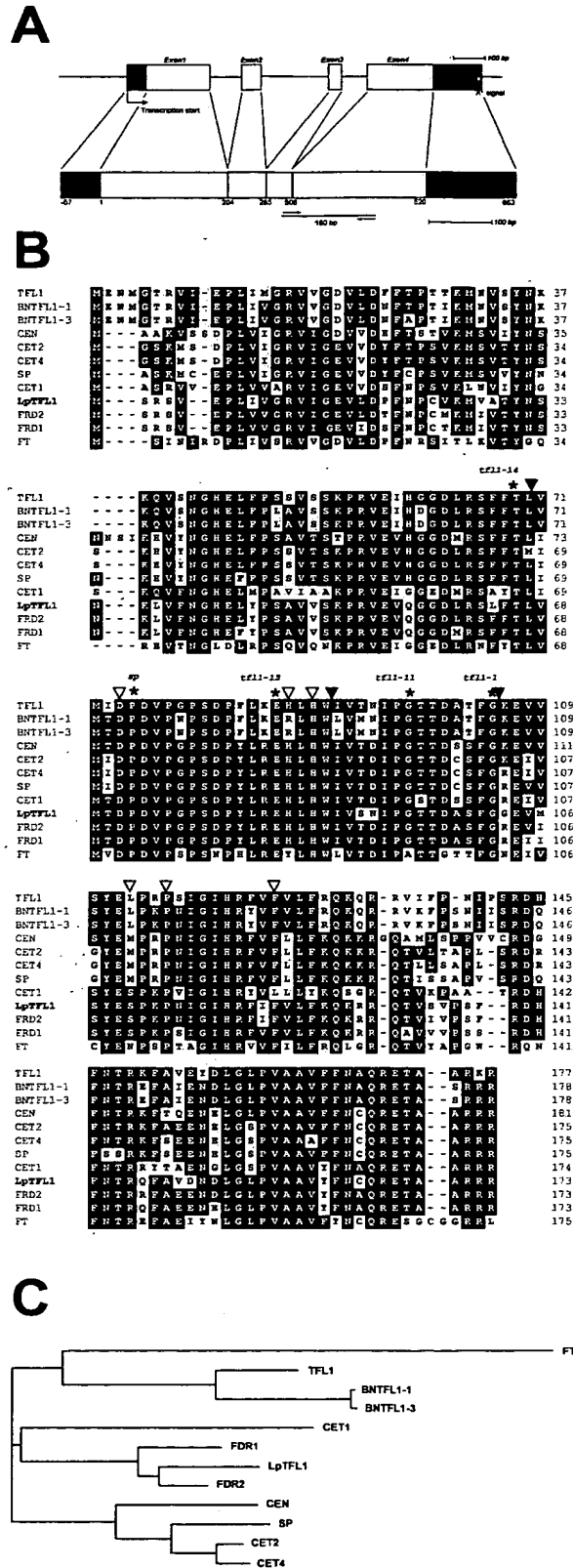


FIGURE 6

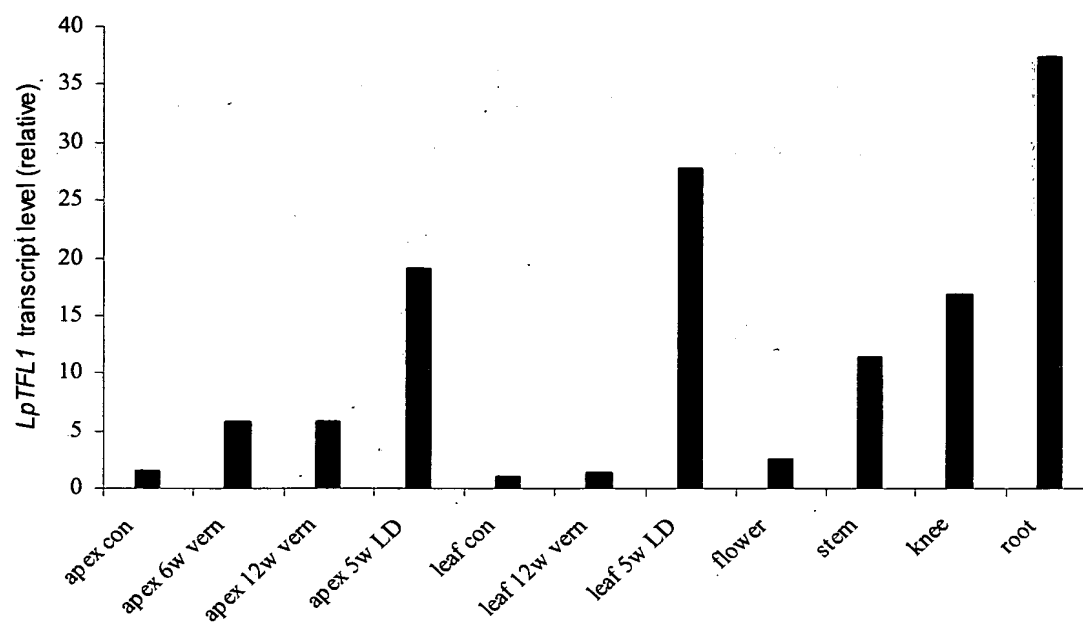


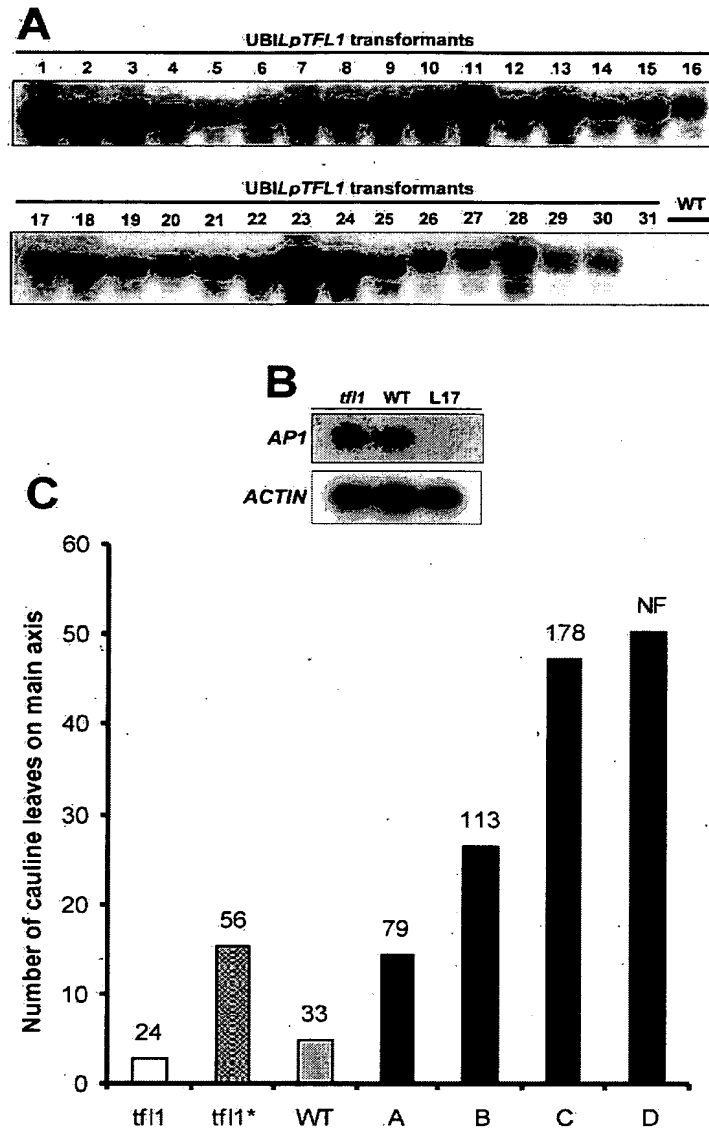
FIGURE 7

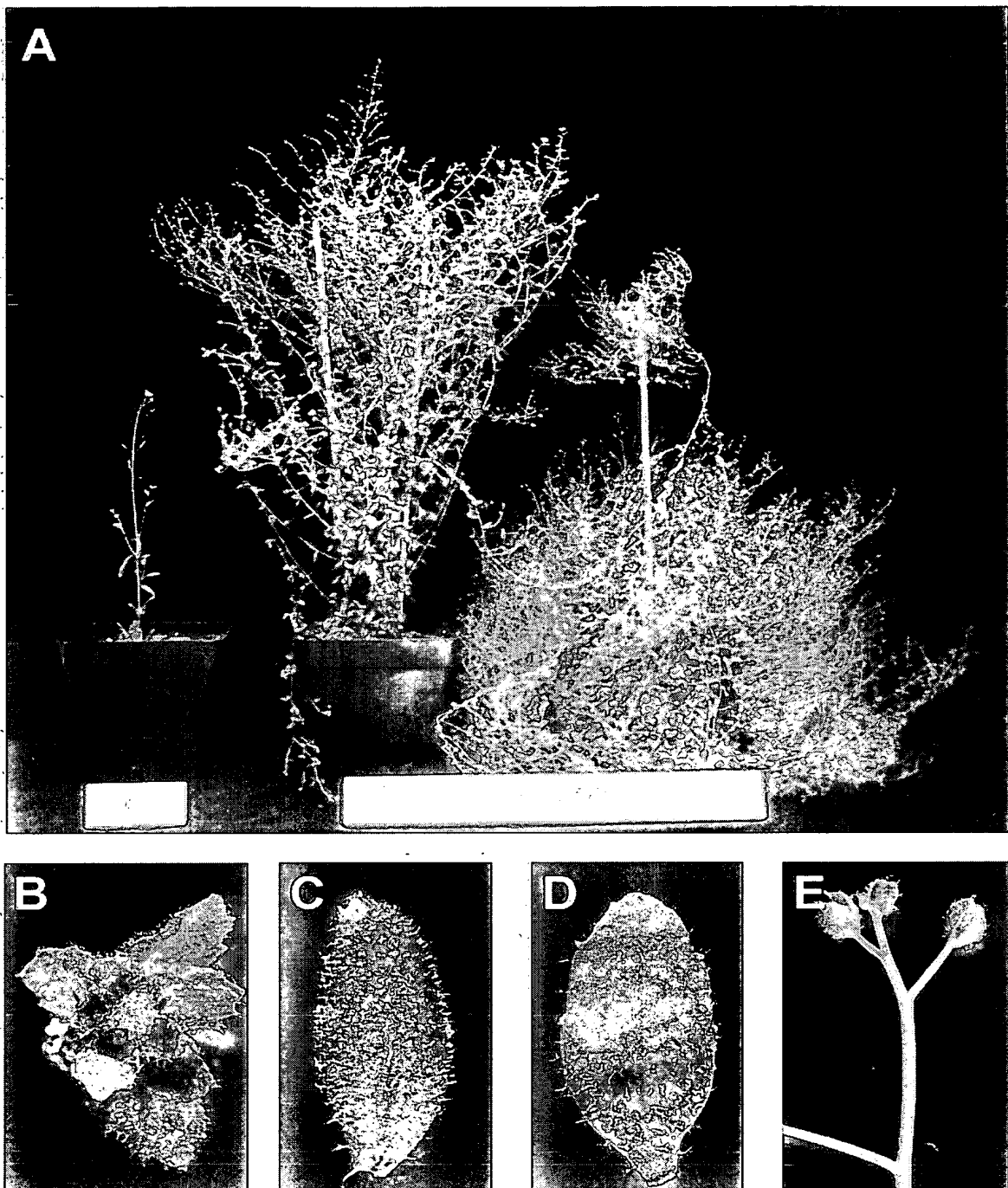
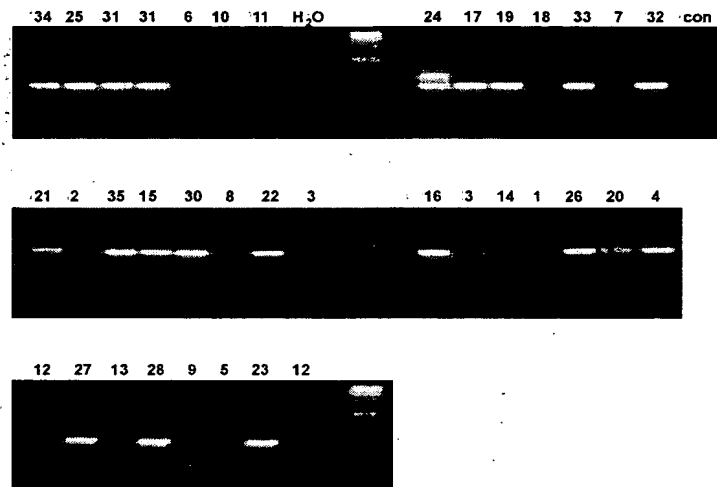
FIGURE 8

FIGURE 9

10/507355

10/15

FIGURE 10

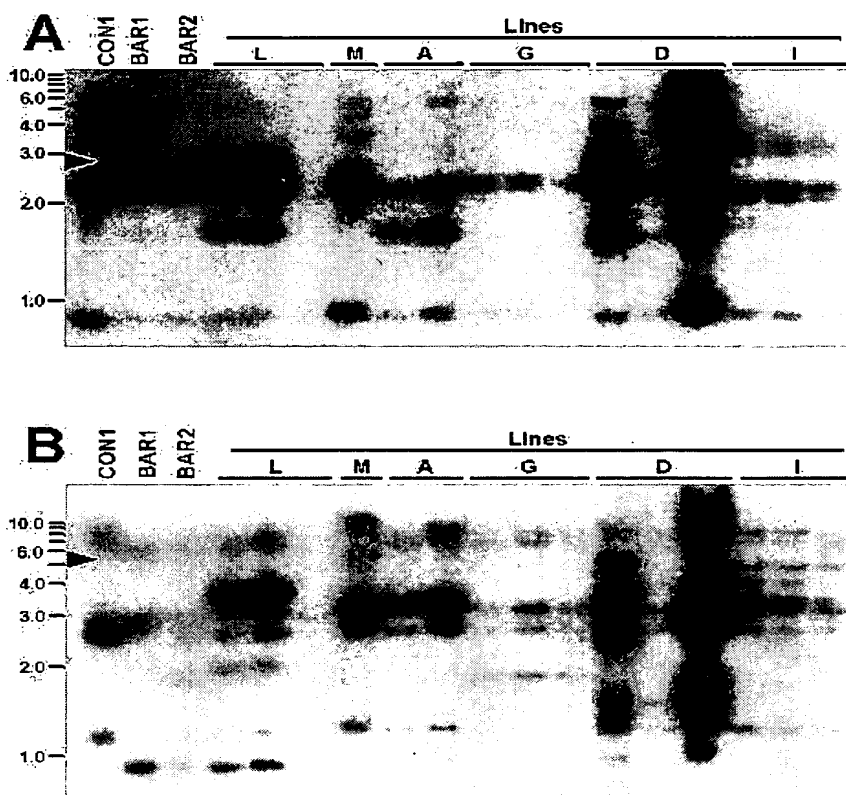
FIGURE 11

FIGURE 12

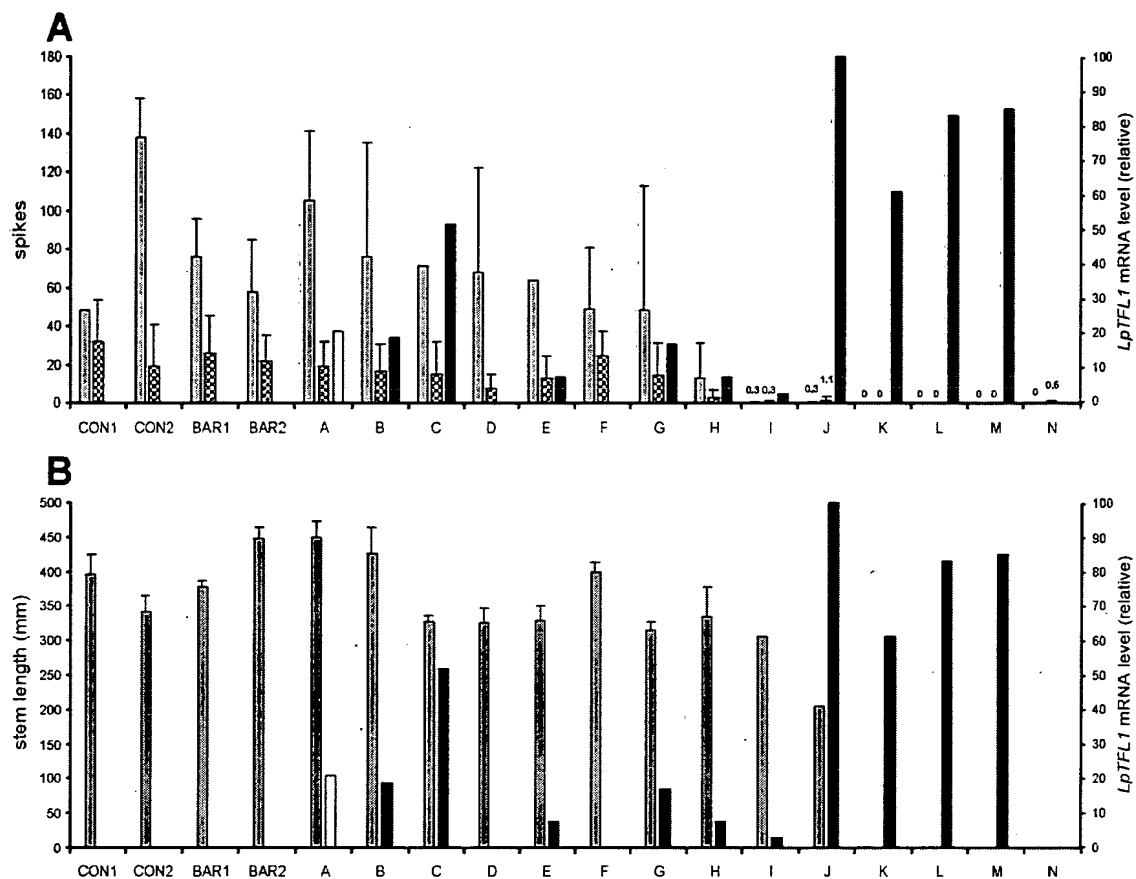


FIGURE 13

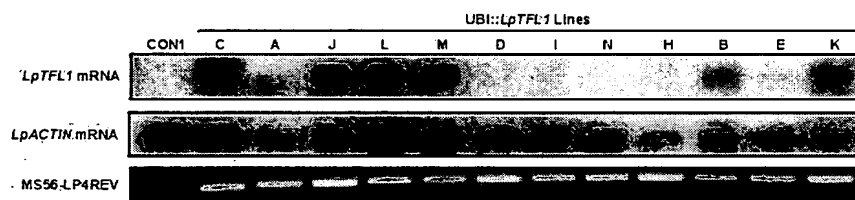


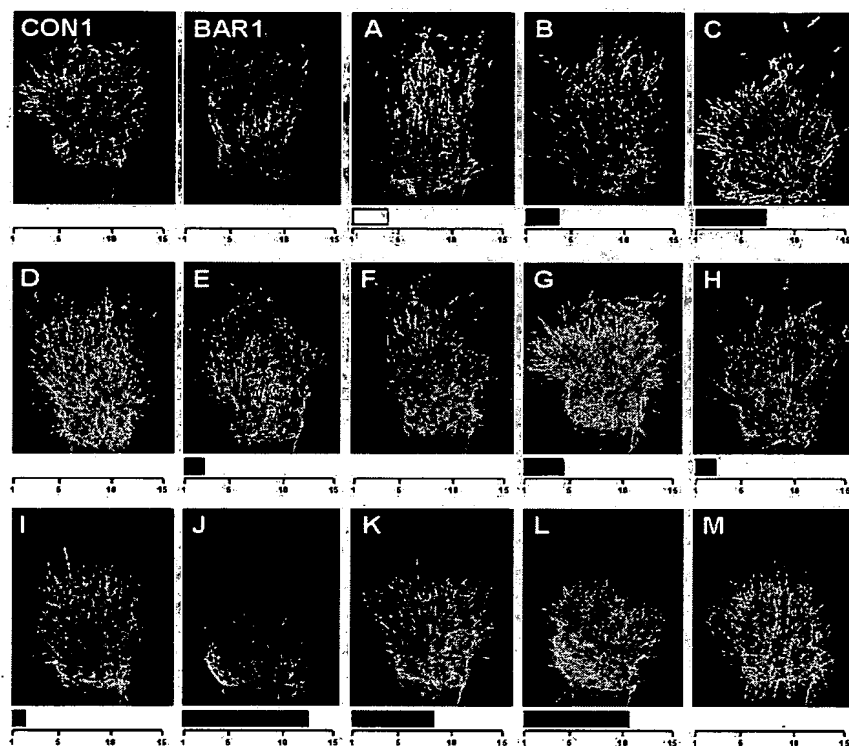
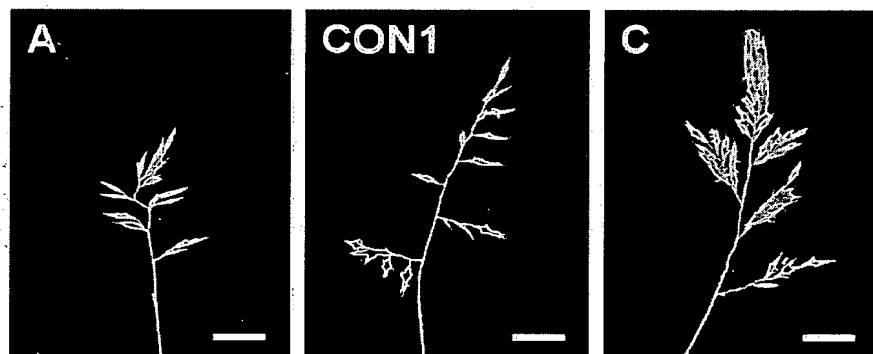
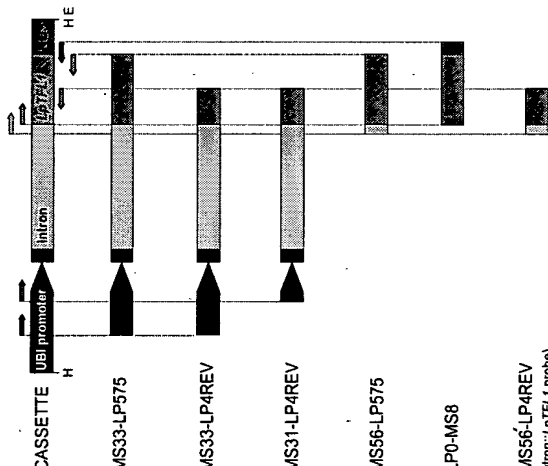
FIGURE 14**FIGURE 15**

FIGURE 16: *Transformation Efficiency and Floral Activity of the Transformants*

Cultivar	Line No.	Inflorescences	PCR	RT-PCR
F6	CON	8	-	-
F6	7	18	-	-
F6	8	11	-	-
F6	17	5,3	+	-
F6	18	13,3	+	-
F6	24	12	+	+
F6	29	0	+	+
F6	32	0	+	+
F6	33	4	+	+
F6	36	0	+	+
ACTION	2	1,8	-	-
ACTION	5	3	-	-
ACTION	9	0,3	-	-
ACTION	12	2	-	-
ACTION	13	0	-	-
ACTION	16	0	+	-
ACTION	19	7,3	+	-
ACTION	21	4	+	+
ACTION	22	0,3	+	+
ACTION	23	0	+	+
ACTION	25	0,3	+	+
ACTION	27	0	+	+
ACTION	28	4	+	+
ACTION	31	0	+	+
ACTION	34	0	+	+
ACTION	35	0	+	+
TELSTAR	1	10	-	-
TELSTAR	3	1	-	-
TELSTAR	4	11,6	-	-
TELSTAR	6	10,8	-	-
TELSTAR	10	5	-	-
TELSTAR	11	3,8	-	-
TELSTAR	14	0	-	-
TELSTAR	15	3,8	+	-
TELSTAR	20	3,5	+	-
TELSTAR	26	0	+	+
TELSTAR	30	3,7	+	+

Figur 17: Transgene integration analysis by PCR using different primer combinations

Primer combination	UBI::LpTFL1 transgenic lines ^a																	
	CASSETTE	CON	BAR	A	B	C	D	E	F	G	H	I	J	K	L	M	N	P
																		
MS33-LP575							0.8						+		+		0.8	2.3
MS33-LP4REV							0.55						+		+		0.55	2.0
MS31-LP4REV				+			+			1.4	+		+		+	+		1.5
MS56-LP575					+	+	+0.5	+		+0.5	+	+	+	+	+	+	+0.5	0.6
LP0-MS8					+	+	+M	+		+	+	+1.8	+	+	+	+	+1.6	0.6
MS56-LP4REV (intron::LpTFL1 probe)				+	+	+	+	+	+	+	+	+	+	+	+	+	+	0.4
Result	Promoter	short					TATA box		short	short		ok	ok	ok	ok	short	TATA box	
	Intron	ok					ok		ok	ok		ok	ok	ok	ok	ok		
	LpTFL1 cDNA	truncated	ok	ok	ok	ok	ok + extra	ok	truncated	ok	ok	ok + extra	ok	ok	ok	ok	ok + extra	

^aplus indicates that the observed fragment had the expected size, whereas numbers indicate that the fragment size deviated from the expected size (numbers in bold), blank field indicates that no PCR-product was detected; E, *EcoRI*; H, *HindIII*

^aplus indicates that the observed fragment had the expected size, whereas numbers indicate that the fragment size deviated from the expected size (numbers in bold), blank field indicates that no PCR-product was detected; E, *EcoRI*; H, *HindIII*

10/507355